



CTGAGCTGACCTGACCCCCAAAGTGAAGGAGAAGCTGCAAGGGAAAAGGGAGGGACAGAT
1 -----+-----+-----+-----+-----+ 60
GACTCGACTGGACTGGGGGTTTCACTTCCTCTTCGACGTTCCCTTTTCCCTCCCTGTCTA
CAGGGAGACCGGGGAAGAAGGAGGAGCAGCCAAGGAGGCTGCTGTCCCCCACAGAGCAG
61 -----+-----+-----+-----+-----+ 120
GTCCCTCTGGCCCCTTCTTCCTCCTCGTCGGTTCCTCCGACGACAGGGGGGTGTCTCGTC
CTCGGACTCAGCTCCCGGAGCAACCCAGCTGCGGAGGCAACGGCAGTGCTGCTCCTCCAG
121 -----+-----+-----+-----+-----+ 180
GAGCCTGAGTCGAGGGCCTCGTTGGGTCGACGCCTCCGTTGCCGTCACGACGAGGAGGTC
CGAAGGACAGCAGGCAGGCAGACAGACAGAGGTCTTGGGACTGGAAGGCCTCAGCCCCCA
181 -----+-----+-----+-----+-----+ 240
GCTTCCTGTCTCGTCCGTCCGTCTGTCTGTCTCCAGGACCTGACCTTCCGGAGTCGGGGGT
GCCACTGGGCTGGGCCTGGCCCAATGGCCTTTAATGACCTCCTGCAGCAGGTGGGGGGTG
241 -----+-----+-----+-----+-----+ 300
CGGTGACCCGACCCGGACCGGGTTACCGGAAATTACTGGAGGACGTCGTCCACCCCCAC
M A F N D L L Q Q V G G V -
TCGGCCGCTTCCAGCAGATCCAGGTCACCCTGGTGGTCCCTCCCCCTGCTCCTGATGGCTT
301 -----+-----+-----+-----+-----+ 360
AGCCGGCGAAGGTCGTCTAGGTCCAGTGGGACCACCAGGAGGGGACGAGGACTACCGAA
G R F Q Q I Q V T L V V L P L L L M A S -
CTCACAACACCCTGCAGAACTTCACTGCTGCCATCCCTACCCACCCTGCCGCCCGCCTG
361 -----+-----+-----+-----+-----+ 420
GAGTGTGTGGGACGTCTTGAAGTGACGACGGTAGGGATGGGTGGTGACGGCGGGCGGAC
H N T L Q N F T A A I P T H H C R P P A -
CCGATGCCAACCCTCAGCAAGAACGGGGGGCTGGAGGTCTGGCTGCCCCGGGACAGGCAGG
421 -----+-----+-----+-----+-----+ 480
GGCTACGGTTGGAGTCGTTCTTGGCCCCCGACCTCCAGACCGACGGGGCCCTGTCCGTCC
D A N L S K N G G L E V W L P R D R Q G -
GGCAGCCTGAGTCCTGCCTCCGCTTCACTCCCCGAGTGGGGACTGCCCTTTCTCAATG
481 -----+-----+-----+-----+-----+ 540
CCGTCCGACTCAGGACGGAGGCGAAGTGGAGGGGCGTCACCCCTGACGGGAAAGAGTTAC
Q P E S C L R F T S P Q W G L P F L N G -
GCACAGAAGCCAATGGCACAGGGGCCACAGAGCCCTGCACCGATGGCTGGATCTATGACA
541 -----+-----+-----+-----+-----+ 600
CGTGTCTTCGGTTACCGTGTCCCCGGTGTCTCGGGACGTGGCTACCGACCTAGATACTGT
T E A N G T G A T E P C T D G W I Y D N -
ACAGCACCTTCCCATCTACCATCGTGAAGTGGGACCTTGTGTGCTCTCACAGGGCCC
601 -----+-----+-----+-----+-----+ 660

FIGURE 1
Sheet 1 of 4

TGTCGTGGAAGGGTAGATGGTAGCACTGACTCACCTGGAACACACGAGAGTGTCCCGGG
 S T F P S T I V T E W D L V C S H R A L -
 TACGCCAGCTGGCCCAGTCCTTGTACATGGTGGGGGTGCTGCTCGGAGCCATGGTGTTCG
 661 -----+-----+-----+-----+-----+ 720
 ATGCGGTTCGACCGGGTCAGGAACATGTACCACCCCCACGACGAGCCTCGGTACCACAAGC
 R Q L A Q S L Y M V G V L L G A M V F G -
 GCTACCTTGCAGACAGGCTAGGCCGCCGGAAGGTACTCATCTTGAACCTACCTGCAGACAG
 721 -----+-----+-----+-----+-----+ 780
 CGATGGAACGTCTGTCCGATCCGGCGGCCTTCCATGAGTAGAACTTGATGGACGTCTGTC
 Y L A D R L G R R K V L I L N Y L Q T A -
 CTGTGTCAGGGACCTGCGCAGCCTTCGCACCCAACTTCCCCATCTACTGCGCCTTCCGGC
 781 -----+-----+-----+-----+-----+ 840
 GACACAGTCCCTGGACGCGTCGGAAGCGTGGGTTGAAGGGGTAGATGACGCGGAAGGCCG
 V S G T C A A F A P N F P I Y C A F R L -
 TCCTCTCGGGCATGGCTCTGGCTGGCATCTCCCTCAACTGCATGACACTGAATGTGGAGT
 841 -----+-----+-----+-----+-----+ 900
 AGGAGAGCCCGTACCGAGACCGACCGTAGAGGGAGTTGACGTACTGTGACTTACACCTCA
 L S G M A L A G I S L N C M T L N V E W -
 GGATGCCCATTACACACGGGCCTGCGTGGGCACCTTGATTGGCTATGTCTACAGCCTGG
 901 -----+-----+-----+-----+-----+ 960
 CCTACGGGTAAAGTGTGTGCCCCGACGCACCCGTGGAACCTAACCGATACAGATGTGCGACC
 M P I H T R A C V G T L I G Y V Y S L G -
 GCCAGTTCCTCCTGGCTGGTGTGGCCTACGCTGTGCCCCACTGGCGCCACCTGCAGCTAC
 961 -----+-----+-----+-----+-----+ 1020
 CGGTCAAGGAGGACCGACCACACCGGATGCGACACGGGGTGACCGCGGTGGACGTGATG
 Q F L L A G V A Y A V P H W R H L Q L L -
 TGGTCTCTGCGCCTTTTTTGCCTTCTTCATCTACTCCTGGTTCTTCATTGAGTCGGCCC
 1021 -----+-----+-----+-----+-----+ 1080
 ACCAGAGACGCGGAAAAAACGGAAGAAGTAGATGAGGACCAAGAAGTAACTCAGCCGGG
 V S A P F F A F F I Y S W F F I E S A R -
 GCTGGCACTCCTCCTCCGGGAGGCTGGACCTCACCTGAGGGCCCTGCAGAGAGTCGCCC
 1081 -----+-----+-----+-----+-----+ 1140
 CGACCGTGAGGAGGAGGCCCTCCGACCTGGAGTGGGACTCCCGGGACGCTCTCAGCGGG
 W H S S S G R L D L T L R A L Q R V A R -
 GGATCAATGGGAAGCGGGAAGAAGGAGCCAAATTGAGTATGGAGGTACTCCGGGCCAGTC
 1141 -----+-----+-----+-----+-----+ 1200

FIGURE 1
 Sheet 2 of 4

CCTAGTTACCCTTCGCCCTTCTTCTCGGTTTAACTCATACCTCCATGAGGCCCGGTCAG
 I N G K R E E G A K L S M E V L R A S L -
 TGCAGAAGGAGCTGACCATGGGCAAAGGCCAGGCATCGGCCATGGAGCTGCTGCGCTGCC
 1201 -----+-----+-----+-----+-----+ 1260
 ACGTCTTCTCGACTGGTACCCGTTTCCGGTCCGTAGCCGGTACCTCGACGACGCGACGG
 Q K E L T M G K G Q A S A M E L L R C P -
 CCACCCTCCGCCACCTCTTCTCTGCCTCTCCATGCTGTGGTTTGCCACTAGCTTTGCAT
 1261 -----+-----+-----+-----+-----+ 1320
 GGTGGGAGGCGGTGGAGAAGGAGACGGAGAGGTACGACACCAAACGGTGATCGAAACGTA
 T L R H L F L C L S M L W F A T S F A Y -
 ACTATGGGCTGGTCATGGACCTGCAGGGCTTTGGAGTCAGCATCTACCTAATCCAGGTGA
 1321 -----+-----+-----+-----+-----+ 1380
 TGATACCCGACCAGTACCTGGACGTCCCGAAACCTCAGTCGTAGATGGATTAGGTCCACT
 Y G L V M D L Q G F G V S I Y L I Q V I -
 TCTTTGGTGCTGTGGACCTGCCTGCCAAGCTTGTGGGCTTCCTTGTCATCAACTCCCTGG
 1381 -----+-----+-----+-----+-----+ 1440
 AGAAACCACGACACCTGGACGGACGGTTCGAACACCCGAAGGAACAGTAGTTGAGGGACC
 F G A V D L P A K L V G F L V I N S L G -
 GTCGCCGGCCTGCCCAGATGGCTGCACTGCTGCTGGCAGGCATCTGCATCCTGCTCAATG
 1441 -----+-----+-----+-----+-----+ 1500
 CAGCGGCCGGACGGGTCTACCGACGTGACGACGACCGTCCGTAGACGTAGGACGAGTTAC
 R R P A Q M A A L L L A G I C I L L N G -
 GGGTGATACCCAGGACCAGTCCATTGTCCGAACCTCTCTTGCTGTGCTGGGGAAGGGTT
 1501 -----+-----+-----+-----+-----+ 1560
 CCCACTATGGGGTCTCTGGTCAGGTAACAGGCTTGGAGAGAACGACACGACCCCTTCCCAA
 V I P Q D Q S I V R T S L A V L G K G C -
 GTCTGGCTGCCTCCTTCAACTGCATCTTCCTGTATACTGGGGAACGTATCCCACAATGA
 1561 -----+-----+-----+-----+-----+ 1620
 CAGACCGACGGAGGAAGTTGACGTAGAAGGACATATGACCCCTTGACATAGGGTGTACT
 L A A S F N C I F L Y T G E L Y P T M I -
 TCCGGCAGACAGGCATGGGAATGGGCAGCACCATGGCCCCGAGTGGGCAGCATCGTGAGCC
 1621 -----+-----+-----+-----+-----+ 1680
 AGGCCGTCTGTCCGTACCCTTACCCGTCTGGTACCGGGCTCACCCGTCTAGCACTCGG
 R Q T G M G M G S T M A R V G S I V S P -
 CACTGGTGAGCATGACTGCCGAGCTCTACCCCTCCATGCCTCTCTTCATCTACGGTGCTG
 1681 -----+-----+-----+-----+-----+ 1740

FIGURE 1
 Sheet 3 of 4

GTGACCACTCGTACTGACGGCTCGAGATGGGGAGGTACGGAGAGAAGTAGATGCCACGAC
 L V S M T A E L Y P S M P L F I Y G A V -
 TTCCTGTGGCCGCCAGCGCTGTCACTGTCTCTCTGCCAGAGACCCTGGGCCAGCCACTGC
 1741 -----+-----+-----+-----+-----+ 1800
 AAGGACACCGGCGGTTCGCGACAGTGACAGGAGGACGGTCTCTGGGACCCGGTCGGTGACG
 P V A A S A V T V L L P E T L G Q P L P -
 CAGACACGGTGCAGGACCTGGAGAGCAGGAAAGGGAAACAGACGCGACAGCAACAAGAGC
 1801 -----+-----+-----+-----+-----+ 1860
 GTCTGTGCCACGTCTCTGGACCTCTCGTCCTTTCCCTTTGTCTGCGCTGTCGTTGTTCTCG
 D T V Q D L E S R K G K Q T R Q Q Q E H -
 ACCAGAAGTATATGGTCCCACTGCAGGCCTCAGCACAAGAGAAGAATGGACTCTGAGGAC
 1861 -----+-----+-----+-----+-----+ 1920
 TGGTCTTCATATAACCAGGGTGACGTCCGGAGTCGTGTTCTTCTTACCTGAGACTCCTG
 Q K Y M V P L Q A S A Q E K N G L *
 TGAGAAGGGGCCTTACAGAACCCTAAAGGGAGGGAAGGTCCTACAGGTCTCCGGCCACCC
 1921 -----+-----+-----+-----+-----+ 1980
 ACTCTTCCCCGGAATGTCTTGGGATTTCCCTCCCTTCCAGGATGTCCAGAGGCCGGTGGG
 ACACAAGGAGGAGGAAGAGGAAATGGTGACCCAAGTGTGGGGGTTGTGGTTCAGGAAAGC
 1981 -----+-----+-----+-----+-----+ 2040
 TGTGTTCTCTCCTTCTCCTTTACCACTGGGTTACACCCCCAACACCAAGTCCTTTTCG
 ATCTTCCCAGGGGTCCACCTCCCTTTATAAACCCACCAGAACCACATCATTAAAAGGTT
 2041 -----+-----+-----+-----+-----+ 2100
 TAGAAGGGTCCCCAGGTGGAGGGAAATATTTGGGGTGGTCTTGGTGTAGTAATTTTCCAA
 TGACTGCGCACCAAAAAAAAAAAAAA
 2101 -----+-----+-----+-----+ 2127
 ACTGACGCGTGGTTTTTTTTTTTTTTT



CTGCACCTGAAGCATTGTTGGTGGGTGAGCAGCATGGGCTTTGAGGAGCTGCTGGAGCAGGT
1 -----+-----+-----+-----+-----+ 60
GACGTGGACTTCGTAAACCACCCACTCGTCGTACCCGAAACTCCTCGACGACCTCGTCCA

M G F E E L L E Q V -

GGGCGGCTTTGGGCCCTTCCAAGTGCAGGATGTGGCACTGCTGGCCCTGCCCCGAGTGCT
61 -----+-----+-----+-----+-----+ 120
CCCCCGAAACCCGGGAAGGTTGACGCCTTACACCGTGACGACCGGGACGGGGCTCAEGA

G G F G P F Q L R N V A L L A L P R V L -

GCTACCACTGCACTTCCTCCTGCCCATCTTCCTGGCTGCCGTGCCTGCCCACCGATGTGC
121 -----+-----+-----+-----+-----+ 180
CGATGGTGACGTGAAGGAGGACGGGTAGAAGGACCGACGGCACGGACGGGTGGCTACACG

L P L H F L L P I F L A A V P A H R C A -

CCTGCCGGGTGCCCCCTGCCAAGTTCAGCCATCAGGATGTGTGGCTGGAGGCCCATCTTCC
181 -----+-----+-----+-----+-----+ 240
GGACGGGCCACGGGGACGGTTGAAGTCGGTAGTCCTACACACCGACCTCCGGGTAGAAGG

L P G A P A N F S H Q D V W L E A H L P -

CCGGGAGCCTGATGGCACGCTCAGCTCCTGCCTCCGCTTTGCCTATCCCCAGGCTCTCCC
241 -----+-----+-----+-----+-----+ 300
GGCCCTCGGACTACCGTGCGAGTCGAGGACGGAGGCGAAACGGATAGGGGTCCGAGAGGG

R E P D G T L S S C L R F A Y P Q A L P -

CAACACCACGTTGGGGGAAGAAAGGCAGAGCCGTGGGGAGCTGGAGGATGAACCTGCCAC
301 -----+-----+-----+-----+-----+ 360
GTTGTGGTGCAACCCCTTCTTTCCGTCTCGGCACCCCTCGACCTCCTACTTGGACGGTG

N T T L G E E R Q S R G E L E D E P A T -

AGTGCCCTGCTCTCAGGGCTGGGAGTACGACCACTCAGAATTCTCCTCTACCATTGCAAC
361 -----+-----+-----+-----+-----+ 420
TCACGGGACGAGAGTCCCGACCCCTCATGCTGGTGAGTCTTAAGAGGAGATGGTAACGTTG

V P C S Q G W E Y D H S E F S S T I A T -

TGAGTGGGATCTGGTGTGTGAGCAGAAAGGTCTGAACAGAGCTGCGTCCACTTTCTTCTT
421 -----+-----+-----+-----+-----+ 480
ACTCACCTAGACCACACACTCGTCTTTCCAGACTTGTCTCGACGCAGGTGAAAGAAGAA

E W D L V C E Q K G L N R A A S T F F F -

CGCCGGTGTGCTGGTGGGGGCTGTGGCCTTTGGATATCTGTCCGACAGGTTTGGGCGGCG
481 -----+-----+-----+-----+-----+ 540
GCGGCCACACGACCACCCCGACACCGGAAACCTATAGACAGGCTGTCCAAACCCGCCGC

A G V L V G A V A F G Y L S D R F G R R -

FIGURE 2

541 CCGTCTGCTGCTGGTAGCCTACGTGAGTACCCTGGTGCTGGGCCTGGCATCTGCAGCCTC 600
 -----+-----+-----+-----+-----+-----+
 CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGACCGTAGACGTCCGAG

 R L L L V A Y V S T L V L G L A S A A S -

 601 CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT 660
 -----+-----+-----+-----+-----+-----+
 GCAGTCGATACATTACAAACGGTAGTGGGCGTGGGAATGACCGAGTCGGGACCGACCAA

 V S Y V M F A I T R T L T G S A L A G F -

 661 TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC 720
 -----+-----+-----+-----+-----+-----+
 ATGGTAGTAGCACTACGGTGACCTCGACCTACCGACCTACACCTCGTGGCGTGGCACCG

 T I I V M P L E L E W L D V E H R T V A -

 721 TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA 780
 -----+-----+-----+-----+-----+-----+
 ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCGCACTACGACGACCGTGACCAACCCAT

 G V L S S T F W T G G V M L L A L V G Y -

 781 CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTCACCCGTCCTTGTGCCCCAAGCAT 840
 -----+-----+-----+-----+-----+-----+
 GGACTATGCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA

 L I R D W R W L L L A V T L P C A P S I -

 841 CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA 900
 -----+-----+-----+-----+-----+-----+
 GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCGGGTACACTT

 L S L W W V P E S A R W L L T Q G H V K -

 901 AGAGGCCCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA 960
 -----+-----+-----+-----+-----+-----+
 TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTCACACACTCCT

 E A H R Y L L H C A R L N G R P V C E D -

 961 CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGGAACGGGTGGTCCGAAGACC 1020
 -----+-----+-----+-----+-----+-----+
 GTCGAAGTCGGTCCCTCCGACACTCGTTTCACCGGCGGCCCCCTTGCCCACCAGGCTTCTGG

 S F S Q E A V S K V A A G E R V V R R P -

 1021 TTCATACCTAGACCTGTTCGACACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT 1080
 -----+-----+-----+-----+-----+-----+
 AAGTATGGATCTGGACAAGGCGTGTGGTGCCGAGGCTGTGTAGAGTGACACGACGCACCA

 S Y L D L F R T P R L R H I S L C C V V -

FIGURE 2

1081 GGTGTGGTTCGGAGTGAACCTTCTCTATTACGGCCTGAGTCTGGATGTGTCTGGGGCTGGG
 -----+-----+-----+-----+-----+-----+ 1140
 CCACACCAAGCCTCACTTGAAGAGGATAATGCCGGACTCAGACCTACACAGCCCCGACCC

 V W F G V N F S Y Y G L S L D V S G L G -

 1141 GCTGAACGTGTACCAGACACAGCTGTTGTTCTGGGGCTGTGGAAGTGCCTCCAAGCTGCT
 -----+-----+-----+-----+-----+-----+ 1200
 CGACTTGACATGGTCTGTGTCTGACAACAAGCCCCGACACCTTGACGGGAGGTTTCGACGA

 L N V Y Q T Q L L F G A V E L P S K L L -

 1201 GGTCTACTTGTCTGGTGCCTACGCAGGACGCCGCTCACGCAAGCCGGGACACTGCTGGG
 -----+-----+-----+-----+-----+-----+ 1260
 CCAGATGAACAGCCACGCGATGCGTCTGCGGCGGAGTGCCTTCGGCCCTGTGACGACCC

 V Y L S V R Y A G R R L T Q A G T L L G -

 1261 CACGGCCCTGGCGTTCGGCACTAGACTGCTAGTGTCTCCGATATGAAGTCCTGGAGCAC
 -----+-----+-----+-----+-----+-----+ 1320
 GTGCCGGGACCGCAAGCCGTGATCTGACGATCACAGGAGGCTATACTTCAGGACCTCGTG

 T A L A F G T R L L V S S D M K S W S T -

 1321 TGTCTGGCAGTGATGGGGAAAGCTTTTCTGAAGCTGCCTTCACCACTGCCTACCTGTT
 -----+-----+-----+-----+-----+-----+ 1380
 ACAGGACCGTCACTACCCCTTTTCGAAAAGACTTCGACGGAAGTGGTGACGGATGGACAA

 V L A V M G K A F S E A A F T T A Y L F -

 1381 CACTTCAGAGTTGTACCCTACGGTGCTCAGACAGACAGGGATGGGGCTGACTGCACTGGT
 -----+-----+-----+-----+-----+-----+ 1440
 GTGAAGTCTCAACATGGGATGCCACGAGTCTGTCTGTCCCTACCCGACTGACGTGACCA

 T S E L Y P T V L R Q T G M G L T A L V -

 1441 GGGCCGGCTGGGGGGCTCTTTGGCCCCACTGGCGGCCTTGCTGGATGGAGTGTGGCTGTC
 -----+-----+-----+-----+-----+-----+ 1500
 CCCGGCCGACCCCCGAGAAACGGGGTGACCGCGGAACGACCTACCTCACACCGACAG

 G R L G G S L A P L A A L L D G V W L S -

 1501 ACTGCCCCAAGCTTACTTATGGGGGGATCGCCCTGCTGGCTGCCGGCACCGCCCTCCTGCT
 -----+-----+-----+-----+-----+-----+ 1560
 TGACGGGTTCGAATGAATACCCCCCTAGCGGGACGACCGACGGCCGTGGCGGGAGGACGA

 L P K L T Y G G I A L L A A G T A L L L -

 1561 GCCAGAGACGAGGCAGGCACAGCTGCCAGAGACCATCCAGGACGTGGAGAGAAAGAGTGC
 -----+-----+-----+-----+-----+-----+ 1620
 CCGTCTCTGCTCCGTCCGTGTCTGACGGTCTCTGGTAGGTCTGCACCTCTCTTTCTCACG

 P E T R Q A Q L P E T I Q D V E R K S A -

FIGURE 2

1621 CCCAACCAGTCTTCAGGAGGAAGAGATGCCCATGAAGCAGGTCCAGAACTAAGTGGGAGT 1680
 -----+-----+-----+-----+-----+
 GGGTTGGTCAGAAGTCCTCCTTCTCTACGGGTACTTCGTCCAGGTCTTGATTACCCCTCA

 P T S L Q E E E M P M K Q V Q N *

 1681 GGAGGCAGGCCCTCCACAGAAGCTCTGCAGCAGGGGCTGGGAGAGCAGAAGGGCAGGCCC 1740
 -----+-----+-----+-----+-----+
 CCTCCGTCCGGGAGGTGTCTTCGAGACGTCGTCCCCGACCCTCTCGTCTTCCCGTCCGGG

 1741 TGCAACTCAGGCTGGGAGTATCGAACCCTCTGCCTAGGGCCGGAGTTGCTGCCAGTACCC 1800
 -----+-----+-----+-----+-----+
 ACGTTGAGTCCGACCCTCATAGCTTGGGAGACGGATCCCGGCCTCAACGACGGTCATGGG

 1801 GCTCCCTCTGCTCATCCATCCTTGATTATTTGGCTTCTAGGAACAGTTGACTTCCCAGAA 1860
 -----+-----+-----+-----+-----+
 CGAGGGAGACGAGTAGGTAGGAACATAAACCAGAGATCCTTGTCAACTGAAGGGTCTT

 1861 TGCAGTGGGCTGCTGGGCACCCCTCTCACGGTTGGGGAGGATTCTGTAAATAAAGGTGCC 1920
 -----+-----+-----+-----+-----+
 ACGTCACCCGACGACCCGTGGGGAGAGTGCCAACCCCTCCTAAGACATTTATTTCCACGG

 1921 CCTTGGGTGGGGCAATGGTGACGAGCTGTGGGAAGAGCCCTGGATAGGAAGCCACTGAG 1980
 -----+-----+-----+-----+-----+
 GGAACCCAACCCCGTTACCACTGCTCGACACCCTTCTCGGGACCTATCCTTCGGTGACTC

 1981 TCTGCCCTGGGCTCTGATAAAACCTTCACCATTAACCTTGCTGTGTGACCTTGGGCATGTG 2040
 -----+-----+-----+-----+-----+
 AGACGGGACCCGAGACTATTTTGGAGTGGAATTGAACGACACACTGGAACCCGTACAC

 2041 GCTTTCCTCTCTGGCCTCAGTCTGTTCATCTCCCAAATGGATAATGAAGCCTCTTGGGA 2100
 -----+-----+-----+-----+-----+
 CGAAAGGGAGAGACCGGAGTCAGACAAGTAGAGGGTTTACCTATTACTTCGGAGAACCCT

 2101 GGCCCTACCATAGGATCTGTTGCCATGCTCAAATGAGTTACTGAATAAGGTGCTTCTGCT 2160
 -----+-----+-----+-----+-----+
 CCGGGATGGTATCCTAGACAACGGTACGAGTTTACTCAATGACTTATTCCACGAAGACGA

 2161 TCTTCTAGAGATGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGC 2220
 -----+-----+-----+-----+-----+
 AGAAGATCTCTACCACGATTTCTTTCCTGATCGTATACTCTGAAGACCATGGTTACCCCG

 2221 TGGTGGGCATGCTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAA 2280
 -----+-----+-----+-----+-----+
 ACCACCCGTACGACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCTGTT

 2281 AAAGAACAGAGCTTTTTGTTCTCATGGCTGGCCCTGCTACCTCCGAGGCACCCCTGCAGGG 2340
 -----+-----+-----+-----+-----+
 TTTCTTGTCTCGAAAAACAAGGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCC

 2341 CAATGCATGTCATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCA 2400
 -----+-----+-----+-----+-----+
 GTTACGTACAGTAGGGTTGGGGGTGTGAGGGGTAGGAGGTTGGGTGACCAGGTACGGGT

FIGURE 2

AAGAAGAGTTGAAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATT
2401 -----+-----+-----+-----+-----+-----+ 2460
TTCTTCTCAACTTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAA
CAATAAACACAAGTTTTATGAGTAAAAAAAAAAAAAAAAAAAA
2461 -----+-----+-----+-----+-----+ 2501
GTTATTTGTGTTCAAATACTCATTTTTTTTTTTTTTTTTTTT

FIGURE 2



CTGCACCTGAAGCATTGGTGGGTGAGCAGCATGGGCTTTGAGGAGCTGCTGGAGCAGGT
1 -----+-----+-----+-----+-----+ 60
GACGTGGACTTCGTAAACCACCCACTCGTCGTACCCGAAACTCCTCGACGACCTCGTCCA

M G F E E L L E Q V -

GGGCGGCTTTGGGGCCCTTCCAACCTGCGGAATGTGGCACTGCTGGCCCTGCCCCGAGTGCT
61 -----+-----+-----+-----+-----+ 120
CCCCCGCAAACCCGGGAAGGTTGACGCCTTACACCGTGACGACCGGGACGGGGCTCACGA

G G F G P F Q L R N V A L L A L P R V L -

GCTACCACTGCACTTCCTCCTGCCCATCTTCCTGGCTGCCGTGCCTGCCCACCGATGTGC
121 -----+-----+-----+-----+-----+ 180
CGATGGTGACGTGAAGGAGGACGGGTAGAAAGGACCGACGGACGGACGGGTGGCTACACG

L P L H F L L P I F L A A V P A H R C A -

CCTGCCGGGTGCCCCCTGCCAACTTCAGCCATCAGGATGTGTGGCTGGAGGCCCATCTTCC
181 -----+-----+-----+-----+-----+ 240
GGACGGCCACGGGGACGGTTGAAGTCGGTAGTCCTACACACCGACCTCCGGGTAGAAGG

L P G A P A N F S H Q D V W L E A H L P -

CCGGGAGCCTGATGGCACGCTCAGCTCCTGCCTCCGCTTTGCCTATCCCCAGGCTCTCCC
241 -----+-----+-----+-----+-----+ 300
GGCCCTCGGACTACCGTGCGAGTCGAGGACGGAGGCGAAACGGATAGGGGTCCGAGAGGG

R E P D G T L S S C L R F A Y P Q A L P -

CAACACCACGTTGGGGGAAGAAAGGCAGAGCCGTGGGGAGCTGGAGGATGAACCTGCCAC
301 -----+-----+-----+-----+-----+ 360
GTTGTGGTGCAACCCCTTCTTTCCGTCTCGGCACCCCTCGACCTCCTACTTGGACGGTG

N T T L G E E R Q S R G E L E D E P A T -

AGTGCCCTGCTCTCAGGGCTGGGAGTACGACCACTCAGAATTCTCCTCTACCATTGCAAC
361 -----+-----+-----+-----+-----+ 420
TCACGGGACGAGAGTCCCCGACCCTCATGCTGGTGAGTCTTAAGAGGAGATGGTAACGTTG

V P C S Q G W E Y D H S E F S S T I A T -

TGAGTGGGATCTGGTGTGTGAGCAGAAAGGTCTGAACAGAGCTGCGTCCACTTTCTTCTT
421 -----+-----+-----+-----+-----+ 480
ACTCACCTAGACCACACACTCGTCTTTCCAGACTTGTCTCGACGCAGGTGAAAGAAGAA

E W D L V C E Q K G L N R A A S T F F F -

CGCCGGTGTGCTGGTGGGGGCTGTGGCCTTTGGATATCTGTCCGACAGGTTTGGGCGGGC
481 -----+-----+-----+-----+-----+ 540
GCGGCCACACGACCACCCCGACACCGAAACCTATAGACAGGCTGTCCAAACCCGCCGC

A G V L V G A V A F G Y L S D R F G R R -

FIGURE 3
Sheet 1 of 4

541 GCGTCTGCTGCTGGTAGCCTACGTGAGTACCCTGGTGCTGGGCCTGGCATCTGCAGCCTC
 -----+-----+-----+-----+-----+-----+ 600
 CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGGACCGTAGACGTCCGAG

 R L L L V A Y V S T L V L G L A S A A S -

 601 CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT
 -----+-----+-----+-----+-----+-----+ 660
 GCAGTCGATACATTACAAACGGTAGTGGGCGTGGGAATGACCGAGTCGGGACCGACCAA

 V S Y V M F A I T R T L T G S A L A G F -

 661 TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC
 -----+-----+-----+-----+-----+-----+ 720
 ATGGTAGTAGCACTACGGTGACCTCGACCTCACCGACCTACACCTCGTGGCGTGGCACCG

 T I I V M P L E L E W L D V E H R T V A -

 721 TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA
 -----+-----+-----+-----+-----+-----+ 780
 ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCGCACTACGACGACCGTGACCAACCCAT

 G V L S S T F W T G G V M L L A L V G Y -

 781 CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTCACCCTGCCTTGTGCCCCAAGCAT
 -----+-----+-----+-----+-----+-----+ 840
 GGACTATGCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA

 L I R D W R W L L L A V T L P C A P S I -

 841 CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA
 -----+-----+-----+-----+-----+-----+ 900
 GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCGGGTACACTT

 L S L W W V P E S A R W L L T Q G H V K -

 901 AGAGGCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA
 -----+-----+-----+-----+-----+-----+ 960
 TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTCCACACTCCT

 E A H R Y L L H C A R L N G R P V C E D -

 961 CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGGAACGGGTGGTCCGAAGACC
 -----+-----+-----+-----+-----+-----+ 1020
 GTCGAAGTCGGTCCCTCCGACACTCGTTTCACCGGCGGCCCTTGCCCAACAGGCTTCTGG

 S F S Q E A V S K V A A G E R V V R R P -

 1021 TTCATACCTAGACCTGTTCCGCACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT
 -----+-----+-----+-----+-----+-----+ 1080
 AAGTATGGATCTGGACAAGGCGTGTGGTGCCGAGGCTGTGTAGAGTGACACGACGCACCA

 S Y L D L F R T P R L R H I S L C C V V -

FIGURE 3
 Sheet 2 of 4

1081 GGTGTGGTTCGGAGTGAACCTTCTCCTATTACGGCCTGAGTCTGGATGTGTCTGGGGCTGGG
 -----+-----+-----+-----+-----+-----+ 1140
 CCACACCAAGCCTCACTTGAAGAGGATAATGCCGGACTCAGACCTACACAGCCCCGACCC

 V W F G V N F S Y Y G L S L D V S G L G -

 1141 GCTGAACGTGTACCAGACACAGCTGTTGTTCTGGGGCTGTGGAAGTGCCTTCCAAGCTGCT
 -----+-----+-----+-----+-----+-----+ 1200
 CGACTTGCACATGGTCTGTGTCTGACAACAAGCCCCGACACCTTGACGGGAGGTTTCGACGA

 L N V Y Q T Q L L F G A V E L P S K L L -

 1201 GGTCTACTTGTCTGGTTCGCTACGCAGGACGCCCTCACGCAAGCCGGGACACTGCTGGG
 -----+-----+-----+-----+-----+-----+ 1260
 CCAGATGAACAGCCACGCGATGCGTCCTGCGGCGGAGTGCCTTCGGCCCTGTGACGACCC

 V Y L S V R Y A G R R L T Q A G T L L G -

 1261 CACGGCCCTGGCGTTCGGCACTAGACTGCTAGTGTCTCCGATATGAAGTCTTGAGCAC
 -----+-----+-----+-----+-----+-----+ 1320
 GTGCCGGGACCGCAAGCCGTGATCTGACGATCACAGGAGGCTATACTTCAGGACCTCGTG

 T A L A F G T R L L V S S D M K S W S T -

 1321 TGTCTTGGCAGTGATGGGGAAAGCTTTTTCTGAAGCTGCCTTCACCACTGCCTACCTGTT
 -----+-----+-----+-----+-----+-----+ 1380
 ACAGGACCGTCACTACCCCTTTGAAAAAGACTTCGACGGAAGTGGTGACGGATGGACAA

 V L A V M G K A F S E A A F T T A Y L F -

 1381 CACTTCAGAGTTGTACCCTACGGTGTCTCAGACAGACAGGGATGGGGCTGACTGCACTGGT
 -----+-----+-----+-----+-----+-----+ 1440
 GTGAAGTCTCAACATGGGATGCCACGAGTCTGTCTGTCCCTACCCCGACTGACGTGACCA

 T S E L Y P T V L R Q T G M G L T A L V -

 1441 GGGCCGGCTGGGGGGCTCTTTGGCCCCACTGGCGGCCTTGCTGGATGGAGTGTGGCTGTC
 -----+-----+-----+-----+-----+-----+ 1500
 CCCGGCCGACCCCCGAGAAACCGGGGTGACCGCCGGAACGACCTACCTCACACCGACAG

 G R L G G S L A P L A A L L D G V W L S -

 1501 ACTGCCCAAGCTTACTTATGGGGGGATCGCCCTGCTGGCTGCCGGCACCGCCCTCCTGCT
 -----+-----+-----+-----+-----+-----+ 1560
 TGACGGGTTTGAATGAATACCCCCCTAGCGGGACGACCGACGGCCGTGGCGGGAGGACGA

 L P K L T Y G G I A L L A A G T A L L L -

 1561 GCCAGAGACGAGGCAGGCACAGCTGCCAGAGACCATCCAGGACGTGGAGAGAAAGAGAGA
 -----+-----+-----+-----+-----+-----+ 1620
 CGGTCTCTGCTCCGTCCGTGTCTGACGGTCTCTGGTAGGTCTGACCTCTCTTTCTCTCT

 P E T R Q A Q L P E T I Q D V E R K R D -

FIGURE 3
 Sheet 3 of 4

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      TGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGCTGGTGGGCATG
1621 -----+-----+-----+-----+-----+-----+ 1680
      ACCACGATTTCTTTCTGATCGTATACTCTGAAGACCATGGTTACCCCGACCACCCGTAC

      G A K E R T S I *

      CTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAAAAGAAGACAGAG
1681 -----+-----+-----+-----+-----+-----+ 1740
      GACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCTGTTTTCTTGTCTC

      CTTTTTGTTCCTCATGGCTGGCCCTGCTACCTCCGAGGCACCCTGCAGGGCAATGCATGTC
1741 -----+-----+-----+-----+-----+-----+ 1800
      GAAAAACAAGGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCCGTTACGTACAG

      ATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCCAAGAAGAGTTG
1801 -----+-----+-----+-----+-----+-----+ 1860
      TAGGGTTGGGGGTGTGAGGGGTAGGAGGTGGGTGACCAGAGTACGGGTTTCTTCTCAAC

      AAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATTCAATAAACACA
1861 -----+-----+-----+-----+-----+-----+ 1920
      TTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAAGTTATTTGTGT

      AGTTTTATGAGTAAAAAAAAAAAAAAAAAAAA
1921 -----+-----+-----+ 1950
      TCAAAATACTCATTTTTTTTTTTTTTTTTTTT

```



GCAGGGACCTCAACTACACTGATCACCAGCCCCATCGGATCCAGACCCGGCCACCAGTGC
1 -----+-----+-----+-----+-----+-----+ 60
CGTCCCTGGAGTTGATGTGACTAGTGGTCGGGTAGCCTAGGTCTGGGCCGGTGGTCACG

CATGACCTTCTCGGAGATCCTGGACCGTGTGGGAAGCATGGGCCATTTCCAGTTCCTGCA
61 -----+-----+-----+-----+-----+-----+ 120
GTACTGGAAGAGCCTCTAGGACCTGGCACACCCTTCGTACCCGGTAAAGGTCAAGGACGT

M T F S E I L D R V G S M G H F Q F L H -

TG TAGCCATACTGGGCCTCCCGATCCTCAACATGGCCAACCACAACCTGCTGCAGATCTT
121 -----+-----+-----+-----+-----+-----+ 180
ACATCGGTATGACCCGGAGGGCTAGGAGTTGTACCGGTTGGTGTGGACGACGTCTAGAA

V A I L G L P I L N M A N H N L L Q I F -

CACAGCCGCCACCCCTGTCCACCACTGTGCCCCGCCCAACAATGCCTCCACAGGGCCTTG
181 -----+-----+-----+-----+-----+-----+ 240
GTGTCGGCGGTGGGGACAGGTGGTGACAGCGGGCGGGGTGTTACGGAGGTGTCCCGGAAC

T A A T P V H H C R P P H N A S T G P W -

GGTGCTCCCCATGGGCCCCAAATGGGAAGCCTGAGAGGTGCCTCCGTTTTGTACATCCGCC
241 -----+-----+-----+-----+-----+-----+ 300
CCACGAGGGGTACCCGGGTTTACCCTTCGGACTCTCCACGGAGGCAAAACATGTAGGCGG

V L P M G P N G K P E R C L R F V H P P -

CAATGCCAGCCTGCCCAATGACACCCAGAGGGCCATGGAGCCATGCCTGGATGGCTGGGT
301 -----+-----+-----+-----+-----+-----+ 360
GTTACGGTCCGACGGGTTACTGTGGGTCTCCCGGTACCTCGGTACGGACCTACCGACCCA

N A S L P N D T Q R A M E P C L D G W V -

CTACAACAGCACCAAGGACTCCATTGTGACAGAGTGGGACTTGGTGTGCAACTCCAACAA
361 -----+-----+-----+-----+-----+-----+ 420
GATGTTGTCTGGTTCCTGAGGTAACACTGTCTCACCCTGAACCACACGTTGAGGTTGTT

Y N S T K D S I V T E W D L V C N S N K -

ACTGAAGGAGATGGCCCAGTCTATCTTCATGGCAGGTATACTGATTGGAGGGCTCGTGCT
421 -----+-----+-----+-----+-----+-----+ 480
TGACTTCCTCTACCGGGTCAGATAGAAGTACCGTCCATATGACTAACCTCCCGAGCACGA

L K E M A Q S I F M A G I L I G G L V L -

TGGAGACCTGTCTGACAGGTTTGGCCGCAGGCCCATCCTGACCTGCAGCTACCTGCTGCT
481 -----+-----+-----+-----+-----+-----+ 540
ACCTCTGGACAGACTGTCCAAACCGGCGTCCGGGTAGGACTGGACGTCGATGGACGACGA

G D L S D R F G R R P I L T C S Y L L L -

GGCAGCCAGCGGCTCCGGTGCAGCCTTCAGCCCCACCTTCCCCATCTACATGGTCTTCCG
541 -----+-----+-----+-----+-----+-----+ 600

FIGURE 4
Sheet 1 of 4

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CCGTCGGTCGCCGAGGCCACGTCGGAAGTCGGGGTGAAGGGGTAGATGTACCAGAAGGC
  A A S G S G A A F S P T F P I Y M V F R -
CTTCCTGTGTGGCTTTGGCATCTCAGGCATTACCCTGAGCACCGTCATCTTGAATGTGGA
601 -----+-----+-----+-----+-----+ 660
GAAGGACACACCGAAACCGTAGAGTCCGTAATGGGACTCGTGGCAGTAGAACTTACACCT
  F L C G F G I S G I T L S T V I L N V E -
ATGGGTGCCTACCCGGATGCGGGCCATCATGTGACAGCACTCGGGTACTGCTACACCTT
661 -----+-----+-----+-----+-----+ 720
TACCCACGGATGGGCCTACGCCCGGTAGTACAGCTGTCTGTGAGCCCATGACGATGTGGAA
  W V P T R M R A I M S T A L G Y C Y T F -
TGGCCAGTTCATTCTGCCCCGGCCTGGCCTACGCCATCCCCCAGTGGCGTTGGCTGCAGTT
721 -----+-----+-----+-----+-----+ 780
ACCGGTCAAGTAAGACGGGCGGACCGGATGCGGTAGGGGGTCACCGCAACCGACGTCAA
  G Q F I L P G L A Y A I P Q W R W L Q L -
AACTGTGTCCATTCCCTTCTTCGTCTTCTTCCTATCATCCTGGTGGACACCAGAGTCCAT
781 -----+-----+-----+-----+-----+ 840
TTGACACAGGTAAGGGAAGAAGCAGAAGAAGGATAGTAGGACCACCTGTGGTCTCAGGTA
  T V S I P F F V F F L S S W W T P E S I -
ACGCTGGTTGGTCTTGTCTGGAAGTCCTCGAAGGCCCTGAAGATACTCCGGCGGGTGGC
841 -----+-----+-----+-----+-----+ 900
TGCGACCAACCAGAACAGACCTTTCAGGAGCTTCCGGGACTTCTATGAGGCCGCCACCG
  R W L V L S G K S S K A L K I L R R V A -
TGTCTTCAATGGCAAGAAGGAAGAGGGAGAAAGGCTCAGCTTGGAGGAGCTCAAACCTCAA
901 -----+-----+-----+-----+-----+ 960
ACAGAAGTTACCGTTCTTCCTTCTCCCTCTTCCGAGTCGAACCTCCTCGAGTTTGAGTT
  V F N G K K E E G E R L S L E E L K L N -
CCTGCAGAAGGAGATCTCCTTGGCCAAGGCCAAGTACACCGCAAGTGACCTGTTCCGGAT
961 -----+-----+-----+-----+-----+ 1020
GGACGTCTTCCTCTAGAGGAACCGGTTCCGGTTCATGTGGCGTTCACTGGACAAGGCCTA
  L Q K E I S L A K A K Y T A S D L F R I -
ACCCATGCTGCGCGCATGACCTTCTGTCTTTCCCTGGCCTGGTTTGCTACCGGTTTTGC
1021 -----+-----+-----+-----+-----+ 1080
TGGGTACGACGCGCGTACTGGAAGACAGAAAGGGACCGGACCAAACGATGGCCAAAACG
  P M L R R M T F C L S L A W F A T G F A -
CTACTATAGTTTGGCTATGGGTGTGGAAGAATTTGGAGTCAACCTCTACATCCTCCAGAT
1081 -----+-----+-----+-----+-----+ 1140

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FIGURE 4
Sheet 2 of 4

GATGATATCAAACCGATACCCACACCTTCTTAAACCTCAGTTGGAGATGTAGGAGGTCTA
 Y Y S L A M G V E E F G V N L Y I L Q I -
 CATCTTTGGTGGGGTCGATGTCCCAGCCAAGTTCATCACCATCCTCTCCTTAAGCTACCT
 1141 -----+-----+-----+-----+-----+ 1200
 GTAGAAACCACCCAGCTACAGGGTCGGTTCAGTAGTGGTAGGAGAGGAATTCGATGGA
 I F G G V D V P A K F I T I L S L S Y L -
 GGGCCGGCATAACCACTCAGGCCGCTGCCCTGCTCCTGGCAGGAGGGGCCATCTTGGCTCT
 1201 -----+-----+-----+-----+-----+ 1260
 CCCGGCCGTATGGTGAGTCCGGCGACGGGACGAGGACCGTCCCTCCCGGTAGAACCAGAGA
 G R H T T Q A A A L L L A G G A I L A L -
 CACCTTTGTGCCCTTGGACTTGCAGACCGTGAGGACAGTATTGGCTGTGTTTGGGAAGGG
 1261 -----+-----+-----+-----+-----+ 1320
 GTGGAAACACGGGAACCTGAACGTCTGGCACTCCTGTGCATAACCGACACAAACCCTTCCC
 T F V P L D L Q T V R T V L A V F G K G -
 ATGCCTATCCAGCTCCTTCAGCTGCCTCTTCCTCTACACAAGTGAATTATACCCACAGT
 1321 -----+-----+-----+-----+-----+ 1380
 TACGGATAGGTCGAGGAAGTCGACGGAGAAGGAGATGTGTTCACTTAATATGGGGTGTCA
 C L S S S F S C L F L Y T S E L Y P T V -
 CATCAGGCAAACAGGTATGGGCGTAAGTAACCTGTGGACCCGCGTGGGAAGCATGGTGTC
 1381 -----+-----+-----+-----+-----+ 1440
 GTAGTCCGTTTGTCCATACCCGCATTTCATTGGACACCTGGGCGCACCCCTTCGTACCACAG
 I R Q T G M G V S N L W T R V G S M V S -
 CCCGCTGGTGAAAATCACGGGTGAGGTACAGCCCTTCATCCCCAATATCATCTACGGGAT
 1441 -----+-----+-----+-----+-----+ 1500
 GGGCGACCACTTTTAGTGCCCACTCCATGTCCGGGAAGTAGGGGTTATAGTAGATGCCCTA
 P L V K I T G E V Q P F I P N I I Y G I -
 CACCGCCCTCCTCGGGGGCAGTGCTGCCCTCTTCCTGCCTGAGACCCTGAATCAGCCCTT
 1501 -----+-----+-----+-----+-----+ 1560
 GTGGCGGGAGGAGCCCCGTCACGACGGGAGAAGGACGGACTCTGGGACTTAGTCGGGAA
 T A L L G G S A A L F L P E T L N Q P L -
 GCCAGAGACTATCGAAGACCTGGAAAACCTGGTCCCTGCGGGCAAAGAAGCCAAAGCAGGA
 1561 -----+-----+-----+-----+-----+ 1620
 CGGTCTCTGATAGCTTCTGGACCTTTTGACCAGGGACGCCCGTTTCTTCGGTTTCGTCT
 P E T I E D L E N W S L R A K K P K Q E -
 GCCAGAGGTGGAAAAGGCCTCCCAGAGGATCCCTCTACAGCCTCACGGACCAGGCCTGGG
 1621 -----+-----+-----+-----+-----+ 1680

FIGURE 4
 Sheet 3 of 4

CGGTCTCCACCTTTTCCGGAGGGTCTCCTAGGGAGATGTCGGAGTGCCTGGTCCGGACCC

P E V E K A S Q R I P L Q P H G P G L G -

CTCCAGCTGAGGACAACGGAACCCCCTTTCCCTGCCCTCCAGAGACTGATCCTAGCCAGG

1681 -----+-----+-----+-----+-----+-----+-----+ 1740

GAGGTCGACTCCTGTTGCCTTGGGGGAAAGGGACGGGAGGTCTCTGACTAGGATCGGTCC

S S *

CACCTTAGGAGTATAGGGAGGCCCCATATAGGTCCATCCTCCTAGGATGAAGCCTTCTGA

1741 -----+-----+-----+-----+-----+-----+-----+ 1800

GTGGAATCCTCATATCCCTCCGGGGTATATCCAGGTAGGAGGATCCTACTTCGGAAGACT

GAGCTTGGTGAAGGTGTCTCCATCACCACCACCAGAGCCTCCTGCCCAGCCCTGGCCAGT

1801 -----+-----+-----+-----+-----+-----+-----+ 1860

CTCGAACCCTTCCACAGAGGTAGTGGTGGTGGTCTCGGAGGACGGGTCGGGACCGGTCA

TCAAAGGTTCAAGCCATCCCTGCCCTTGTCTCCCTGCAACCCAAGCCCTGCCATTCTTC

1861 -----+-----+-----+-----+-----+-----+-----+ 1920

AGTTTCCAAGTTCGGTAGGGACGGGAACAAGAGGGACGTTGGGTTTCGGGACGGTAAGAAG

TGTCTAGCCCTTCCCCACTGGCCAACTTCCCCCACTGTCCCGGTCCCTCTTCCCCTGAGGT

1921 -----+-----+-----+-----+-----+-----+-----+ 1980

ACAGATCGGGAAGGGGTGACCGGTTGAAGGGGGTGACAGGGCCAGGAGAAGGGGACTCCA

CCCCTGATATCCCCTGGCTCAGTCCTAACAAGACTGAGTCTTAACAAGATGAGAAGTCCT

1981 -----+-----+-----+-----+-----+-----+-----+ 2040

GGGGACTATAGGGGACCGAGTCAGGATTGTTCTGACTCAGAAATTGTTCTACTCTTCAGGA

CCCCTTCTTGCTCCACACTTTTCTTTGATGGGAGGTTTCAATAAACAGCGATAAGAAC

2041 -----+-----+-----+-----+-----+-----+-----+ 2100

GGGGAAGAACGGAGGGTGTGAAAAGAACTACCCTCCAAAGTTATTTGTCGCTATTCTTG

TCTAAAAAAAAAAAAAAAAAAAA

2101 -----+-----+-----+-----+-----+-----+-----+ 2121

AGATTTTTTTTTTTTTTTTTTTT



CAAATTATTTCTTACGTGACTTTAGAGAAAACGGCTACCTATCTGACCCCAAAACGACTT
1 -----+-----+-----+-----+-----+ 60
GTTTAATAAAGAATGCACTGAAATCTCTTTTGCCGATGGATAGACTGGGGTTTTGCTGAA

GAGGAAACTGTTTCCACGGTCCTGCTGCAGGGGGGAAGCACAGTCGTCAAGAAGAGAGTG
61 -----+-----+-----+-----+-----+ 120
CTCCTTTGACAAAGGTGCCAGGACGACGTCCCCCTTCGTGTCAGCAGTTCTTCTCTCAC

GGGTCAGGATCAAAACACATTTAGTGTGACTTAGGGAAAGAAAACATTTTCCCTCTTTGA
121 -----+-----+-----+-----+-----+ 180
CCCAGTCCTAGTTTTGTGTAAATCACACTGAATCCCTTTCTTTTGTAAGGAGAGAACT

ACCTCTCTGGATACAGTCATTTTGCCTCTACTTGAGGATCAACTGTTCAACCTCAATGGC
181 -----+-----+-----+-----+-----+ 240
TGGAGAGACCTATGTCAGTAAACGGAGATGAACTCCTAGTTGACAAGTTGGAGTTACCG

M A -

CTTTCAGGACCTCCTGGGTCACGCTGGTGACCTGTGGAGATTCCAGATCCTTCAGACTGT
241 -----+-----+-----+-----+-----+ 300
GAAAGTCCTGGAGGACCCAGTGCGACCACTGGACACCTCTAAGGTCTAGGAAGTCTGACA

F Q D L L G H A G D L W R F Q I L Q T V -

TTTTCTCTCAATCTTTGCTGTTGCTACATACCTTCATTTTATGCTGGAGAAGTTCACTGC
301 -----+-----+-----+-----+-----+ 360
AAAAGAGAGTTAGAAACGACAACGATGTATGGAAGTAAAATACGACCTCTTGAAGTGACG

F L S I F A V A T Y L H F M L E N F T A -

ATTCATACCTGGCCATCGCTGCTGGGTCCACATCCTGGACAATGACACTGTCTCTGACAA
361 -----+-----+-----+-----+-----+ 420
TAAGTATGGACCGGTAGCGACGACCCAGGTGTAGGACCTGTTACTGTGACAGAGACTGTT

F I P G H R C W V H I L D N D T V S D N -

TGACACTGGGGCCCTCAGCCAAGATGCACTCTTGAGAATCTCCATCCCACTGGACTCAAA
421 -----+-----+-----+-----+-----+ 480
ACTGTGACCCCGGGAGTCGGTTCTACGTGAGAACTCTTAGAGGTAGGGTGACCTGAGTTT

D T G A L S Q D A L L R I S I P L D S N -

CATGAGGCCAGAGAAGTGTGCTGCTTTGTTTCATCCTCAGTGGCAGCTCCTTCACCTGAA
481 -----+-----+-----+-----+-----+ 540
GTACTCCGGTCTCTTCACAGCAGCGAAACAAGTAGGAGTCACCGTCGAGGAAGTGGACTT

M R P E K C R R F V H P Q W Q L L H L N -

TGGGACCTTCCCCAACACAAGTGACGCAGACATGGAGCCCTGTGTGGATGGCTGGGTGTA
541 -----+-----+-----+-----+-----+ 600
ACCCTGGAAGGGGTTGTGTTCACTGCGTCTGTACCTCGGGACACACCTACCGACCCACAT

G T F P N T S D A D M E P C V D G W V Y -

FIGURE 5
Sheet 1 of 4

TGACAGAATCTCCTTCTCATCCACCATCGGTGACCTGAAGTGGGATCTGGTATGTGACTC
 601 -----+-----+-----+-----+-----+-----+ 660
 ACTGTCTTAGAGGAAGAGTAGGTGGTAGCCACTGGACTTCACCCTAGACCATACACTGAG

 D R I S F S - S T I G D L K W D L V C D S -

 TCAATCACTGACTTCAGTGGCTAAATTTGTATTCATGGCTGGAATGATGTTGGGAGGCAT
 661 -----+-----+-----+-----+-----+-----+ 720
 AGTTAGTGACTGAAGTCACCGATTAAACATAAGTACCGACCTTACTACAACCCCTCCGTA

 Q S L T S V A K F V F M A G M M L G G I -

 CTTAGGCGTTCAATTTATCAGACAGGTTTGGGAGAAGTTTCGTGCTCAGATGGTGTTACCT
 721 -----+-----+-----+-----+-----+-----+ 780
 GAATCCGCAAGTAAATAGTCTGTCCAAACCCCTCTTCAAAGCACGAGTCTACCACAATGGA

 L G V H L S D R F G R S F V L R W C Y L -

 CCAGGTTGCCATTGTTGGCACTTGTGCAGCGTTGGCTCCCACCTTCCTCATTACTGCTC
 781 -----+-----+-----+-----+-----+-----+ 840
 GGTCCAACGGTAACAACCGTGAACACGTCGCAACCGAGGGTGAAAGGAGTAAATGACGAG

 Q V A I V G T C A A L A P T F L I Y C S -

 AGTACGCTTCTTGTCTGGGATTGCTGCAATGAGCTTCATAACAAATACTATTATGTTAAT
 841 -----+-----+-----+-----+-----+-----+ 900
 TCATGCGAAGAACAGACCCTAACGACGTTACTCGAAGTATTGTTTATGATAATACAATTA

 V R F L S G I A A M S F I T N T I M L I -

 AGCCGAGTGGGCAACACACAGATTCCAGGCCATGGGAATTACATTGGGAATGTGCCCTTC
 901 -----+-----+-----+-----+-----+-----+ 960
 TCGGCTCACCCGTTGTGTCTAAGGTCCGGTACCCTTAATGTAACCCCTACACGGGAAG

 A E W A T H R F Q A M G I T L G M C P S -

 TGGTATTGCATTTATGACCCTGGCAGGCCTGGCTTTTGCCATTCGAGACTGGCATATCCT
 961 -----+-----+-----+-----+-----+-----+ 1020
 ACCATAACGTAAATACTGGGACCGTCCGGACCGAAAAACGGTAAGCTCTGACCGTATAGGA

 G I A F M T L A G L A F A I R D W H I L -

 CCAGCTGGTGGTGTCTGTACCATACTTTGTGATCTTTCTGACCTCAAGTTGGCTGCTAGA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GGTCGACCACCACAGACATGGTATGAAACACTAGAAAGACTGGAGTTCAACCGACGATCT

 Q L V V S V P Y F V I F L T S S W L L E -

 GTCTGCTCGGTGGCTCATTATCAACAATAAACAGAGGAAGGCTTAAAGGAACTTAGAAA
 1081 -----+-----+-----+-----+-----+-----+ 1140
 CAGACGAGCCACCGAGTAATAGTTGTTATTTGGTCTCCTTCCGAATTTCTTGAATCTTT

 S A R W L I I N N K P E E G L K E L R K -

FIGURE 5
 Sheet 2 of 4

AGCTGCACACAGGAGTGGAAATGAAGAATGCCAGAGACACCCTAACCCCTGGAGATTTTGAA
 1141 -----+-----+-----+-----+-----+ 1200
 TCGACGTGTGTCCTCACCTTACTTCTTACGGTCTCTGTGGGATTGGGACCTCTAAAACTT

 A A H R S G M K N A R D T L T L E I L K -

 ATCCACCATGAAAAAAGAACTGGAGGCAGCACAAAAAAAACCTTCTCTGTGTGAAAT
 1201 -----+-----+-----+-----+-----+ 1260
 TAGGTGGTACTTTTTTCTTGACCTCCGTCGTGTTTTTTTTTTTGGGAAGAGACACACTTTA

 S T M K K E L E A A Q K K K P S L C E M -

 GCTCCACATGCCCCAACATATGTAAAAGGATCTCCCTCCTGTCCTTTACGAGATTTGCAAA
 1261 -----+-----+-----+-----+-----+ 1320
 CGAGGTGTACGGGTTGTATACATTTTCTAGAGGGAGGACAGGAAATGCTCTAAACGTTT

 L H M P N I C K R I S L L S F T R F A N -

 CTTTATGGCCTATTTTGGCCTTAATCTCCATGTCCAGCATCTGGGGAACAATGTTTTCTT
 1321 -----+-----+-----+-----+-----+ 1380
 GAAATACCGGATAAAAACCGGAATTAGAGGTACAGGTCGTAGACCCCTTGTTACAAAAGGA

 F M A Y F G L N L H V Q H L G N N V F L -

 GTTGCAGACTCTCTTTGGTGCAGTCATCCTCCTGGCCAACTGTGTTGCACCTTGGGCACT
 1381 -----+-----+-----+-----+-----+ 1440
 CAACGTCTGAGAGAAACCACGTCAGTAGGAGGACCGGTTGACACAACGTGGAACCCGTGA

 L Q T L F G A V I L L A N C V A P W A L -

 GAAATACATGAACCGTCGAGCAAGCCAGATGCTTCTCATGTTCTACTGGCAATCTGCCT
 1441 -----+-----+-----+-----+-----+ 1500
 CTTTATGTACTTGGCAGCTCGTTCCGTCTACGAAGAGTACAAGGATGACCGTTAGACGGA

 K Y M N R R A S Q M L L M F L L A I C L -

 TCTGGCCATCATATTTGTGCCACAAGAAATGCAGACGCTGCGTGAGGTTTTGGCAACACT
 1501 -----+-----+-----+-----+-----+ 1560
 AGACCGGTAGTATAAACACGGTGTTCTTTACGTCTGCGACGCACTCCAAAACCGTTGTGA

 L A I I F V P Q E M Q T L R E V L A T L -

 GGGCTTAGGAGCGTCTGCTCTTGCCAATACCCTTGCTTTTGCCCATGGAAATGAAGTAAT
 1561 -----+-----+-----+-----+-----+ 1620
 CCCGAATCCTCGCAGACGAGAACGGTTATGGGAACGAAAACGGGTACCTTTACTTCATTA

 G L G A S A L A N T L A F A H G N E V I -

 TCCCACCATAATCAGGGCAAGAGCTATGGGGATCAATGCAACCTTTGCTAATATAGCAGG
 1621 -----+-----+-----+-----+-----+ 1680
 AGGGTGGTATTAGTCCCGTTCTCGATACCCCTAGTTACGTTGGAACGATTATATCGTCC

 P T I I R A R A M G I N A T F A N I A G -

FIGURE 5
 Sheet 3 of 4

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AGCCCTGGCTCCCCTCATGATGATCCTAAGTGTGTATTCTCCACCCCTGCCCTGGATCAT
1681 -----+-----+-----+-----+-----+-----+ 1740
TCGGGACCGAGGGGAGTACTACTAGGATTCACACATAAGAGGTGGGGACGGGACCTAGTA

  A  L  A  P  L  M  M  I  L  S  V  Y  S  P  P  L  P  W  I  I  -

CTATGGAGTCTTCCCCTTCATCTCTGGCTTTGCTTTCTCCTCCTTCCTGAAACCAGGAA
1741 -----+-----+-----+-----+-----+-----+ 1800
GATACCTCAGAAGGGGAAGTAGAGACCGAAACGAAAGGAGGAGGAAGGACTTTGGTCCTT

  Y  G  V  F  P  F  I  S  G  F  A  F  L  L  L  P  E  T  R  N  -

CAAGCCTCTGTTTGACACCATCCAGGATGAGAAAAATGAGAGAAAAGACCCAGAGAACC
1801 -----+-----+-----+-----+-----+-----+ 1860
GTTTCGGAGACAAACTGTGGTAGGTCCTACTCTTTTTACTCTCTTTTCTGGGGTCTCTTGG

  K  P  L  F  D  T  I  Q  D  E  K  N  E  R  K  D  P  R  E  P  -

AAAGCAAGAGGATCCGAGAGTGAAGTGACGCAGTTTTAAGGAATTCAGGAGCTGACTG
1861 -----+-----+-----+-----+-----+-----+ 1920
TTTCGTTCTCCTAGGCTCTCACCTTCACTGCGTCAAAATTCCTTAAGGTCCTCGACTGAC

  K  Q  E  D  P  R  V  E  V  T  Q  F  *

CCGATCAATGAGCCAGATGAAGGGAACAATCAGGACTATTCCTAGACACTAGCAAAA
1921 -----+-----+-----+-----+-----+-----+ 1977
GGCTAGTTACTCGGTCTACTTCCCTTGTTAGTCCTGATAAGGATCTGTGATCGTTTT

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CTCCTGATAGCAAAAGAACTGAGGAAGCTCTTTCCACTACGGCTGTATTGCACTGGTGAG
1 -----+-----+-----+-----+-----+-----+ 60
GAGGACTATCGTTTTCTTGACTCCTTCGAGAAAGGTGATGCCGACATAACGTGACCACTC
TCCGGGCCCCATGGATGAGAAATTGATGCGAGGATCAATACAAGCTTAATTTGAATTAATA
61 -----+-----+-----+-----+-----+-----+ 120
AGGCCCGGGTACCTACTCTTTAACTACGCTCCTAGTTATGTTTCAATTAACTTAATTAT
AAAGGAAATATTTTCTCCCTTTGAACTTATCTCCGTAAAGCCATTGTGCCTCCTCTTGGG
121 -----+-----+-----+-----+-----+-----+ 180
TTTCCTTTATAAAAGAGGGGAACTTGAATAGAGGCATTTTCGGTAACACGGAGGAGAACCC
GGTCACGTGTTTACAATCAATGGCCTTTGAGGAGCTCTTGAGTCAAGTTGGAGGCCTTGG
181 -----+-----+-----+-----+-----+-----+ 240
CCAGTGCACAAGTGTTAGTTACCGGAACTCCTCGAGAACTCAGTTCAACCTCCGGAACC
M A F E E L L S Q V G G L G -
GAGATTTTCAGATGCTTCATCTGGTTTTTATTCTTCCCTCTCTCATGTTATTAATCCCTCA
241 -----+-----+-----+-----+-----+-----+ 300
CTCTAAAGTCTACGAAGTAGACCAAAAATAAGAAGGGAGAGAGTACAATAATTAGGGAGT
R F Q M L H L V F I L P S L M L L I P H -
TATACTGCTAGAGAACTTTGCTGCAGCCATTCCTGGTCATCGTTGCTGGGTCCACATGCT
301 -----+-----+-----+-----+-----+-----+ 360
ATATGACGATCTCTTGAACGACGTCGGTAAGGACCAGTAGCAACGACCCAGGTGTACGA
I L L E N F A A A I P G H R C W V H M L -
GGACAATAATACTGGATCTGGTAATGAACTGGAATCCTCAGTGAAGATGCCCTCTTGAG
361 -----+-----+-----+-----+-----+-----+ 420
CCTGTTATTATGACCTAGACCATTACTTTGACCTTAGGAGTCACTTCTACGGGAGAACTC
D N N T G S G N E T G I L S E D A L L R -
AATCTCTATCCCACTAGACTCAAATCTGAGGCCAGAGAAGTGTCGTCGCTTTGTCCATCC
421 -----+-----+-----+-----+-----+-----+ 480
TTAGAGATAGGGTGATCTGAGTTTAGACTCCGGTCTCTTCACAGCAGCGAAACAGGTAGG
I S I P L D S N L R P E K C R R F V H P -
CCAGTGGCAGCTTCTTCACCTGAATGGGACTATCCACAGCACAAGTGAGGCAGACACAGA
481 -----+-----+-----+-----+-----+-----+ 540
GGTCACCGTCGAAGAAGTGGACTTACCCTGATAGGTGTCGTGTTCACTCCGTCTGTGTCT
Q W Q L L H L N G T I H S T S E A D T E -
ACCCTGTGTGGATGGCTGGGTATATGATCAAAGCTACTTCCCTTCGACCATTGTGACTAA
541 -----+-----+-----+-----+-----+-----+ 600
TGGGACACACCTACCGACCCATATACTAGTTTCGATGAAGGGAAGCTGGTAACACTGATT
P C V D G W V Y D Q S Y F P S T I V T K -

FIGURE 6
Sheet 1 of 5

GTGGGACCTGGTATGTGATTATCAGTCACTGAAATCAGTGGTTCAATTCCTACTTCTGAC
 601 -----+-----+-----+-----+-----+ 660
 CACCTGGACCATACTAATAAGTACAGTCACTTTAGTCACCAAGTTAAGGATGAAGACTG

 W D L V C D Y Q S L K S V V Q F L L L T -

 TGAATGCTGGTGGGAGGCATCATAGGTGGCCATGTCTCAGACAGGTTTGGGCGAAGATT
 661 -----+-----+-----+-----+-----+ 720
 ACCTTACGACCACCCTCCGTAGTATCCACCGGTACAGAGTCTGTCCAAACCCGCTTCTAA

 G M L V G G I I G G H V S D R F G R R F -

 TATTCTCAGATGGTGTGTTGCTCCAGCTTGCCATTACTGACACCTGCGCTGCCTTCGCTCC
 721 -----+-----+-----+-----+-----+ 780
 ATAAGAGTCTACCACAAACGAGGTGCAACGGTAATGACTGTGGACGCGACGGAAGCGAGG

 I L R W C L L Q L A I T D T C A A F A P -

 CACCTTCCCTGTTTACTGTGTACTACGCTTCTTGGCAGGTTTTTCTTCCATGATCATTAT
 781 -----+-----+-----+-----+-----+ 840
 GTGGAAGGGACAAATGACACATGATGCGAAGAACCGTCCAAAAGAAGGTACTAGTAATA

 T F P V Y C V L R F L A G F S S M I I I -

 ATCAAATAATTCTTTGCCATTACTGAGTGGATAAGGCCCAACTCTAAAGCCCTGGTAGT
 841 -----+-----+-----+-----+-----+ 900
 TAGTTTATTAAGAAACGGGTAATGACTCACCTATTCCGGGTGAGATTTCCGGGACCATCA

 S N N S L P I T E W I R P N S K A L V V -

 AATATTGTCATCTGGTGGCCCTTAGTATTGGACAGATAATCCTGGGAGGCTTGGCTTATGT
 901 -----+-----+-----+-----+-----+ 960
 TTATAACAGTAGACCACGGGAATCATAACCTGTCTATTAGGACCCTCCGAACCGAATACA

 I L S S G A L S I G Q I I L G G L A Y V -

 CTTCCGAGACTGGCAAACCCTGCACGTGGTGGCGTCAGTACCTTTCCTTGGCCTCCTTCT
 961 -----+-----+-----+-----+-----+ 1020
 GAAGGCTCTGACCGTTTGGGACGTGCACCACCGCAGTCATGGAAAGGAACCGGAGGAAGA

 F R D W Q T L H V V A S V P F L G L L L -

 CCTTCAAAGGTGGCTGGTGGGAATCTGCTCGGTGGTTGATAATCACCAATAAACTAGATGA
 1021 -----+-----+-----+-----+-----+ 1080
 GGAAGTTTCCACCGACCACCTTAGACGAGCCACCAACTATTAGTGGTTATTTGATCTACT

 L Q R W L V E S A R W L I I T N K L D E -

 GGGCTTAAAGGCACTTAGAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAAC
 1081 -----+-----+-----+-----+-----+ 1140
 CCCGAATTTCCGTGAATCTTTTCAACGTGCGTGTTTACCTTATTTCTTACGACTTCTTTG

 G L K A L R K V A R T N G I K N A E E T -

FIGURE 6
 Sheet 2 of 5

1141 CCTGAACATAGAGGTTGTAAGATCCACCATGCAGGAGGAGCTGGATGCAGCACAGACCAA + 1200
 GGACTTGTATCTCCAACATTCTAGGTGGTACGTCTCTCGACCTACGTCTGTCTGGTT
 L N I E V V R S T M Q E E L D A A Q T K -
 1201 AACTACTGTGTGTGACTTGTTCGCAACCCCAGTATGCGTAAAAGGATCTGTATCCTGGT + 1260
 TTGATGACACACACTGAACAAGGCGTTGGGGTCATACGCATTTTCCTAGACATAGGACCA
 T T V C D L F R N P S M R K R I C I L V -
 1261 ATTTTGTAGATTTGCAAACACAATACCTTTTATGGTACCATGGTCAATCTTCAGCATGT + 1320
 TAAAACTCTAAACGTTTGTGTTATGGAAAAATACCATGGTACCAGTTAGAAGTCGTACA
 F L R F A N T I P F Y G T M V N L Q H V -
 1321 GGGGAGCAACATTTTCCTGTTGCAGGTACTTTATGGAGCTGTCGCTCTCATAGTTCGATG + 1380
 CCCCTCGTTGTAAAAGGACAACGTCCATGAAATACCTCGACAGCGAGAGTATCAAGCTAC
 G S N I F L L Q V L Y G A V A L I V R C -
 1381 TCTTGCTCTTTTGACACTAAATCATATGGGGCCGTCGAATAAGCCAGATATTGTTTCATGTT + 1440
 AGAACGAGAAAACGTGTGATTTAGTATACCCGGCAGCTTATTCGGTCTATAACAAGTACAA
 L A L L T L N H M G R R I S Q I L F M F -
 1441 CCTGGTGGGCCTTTCCATTTTGGCCAACACGTTTGTGCCCCAAGAAATGCAGACCCTGCG + 1500
 GGACCACCCGGAAAGGTAAAACCGGTTGTGCAAAACACGGGTTTCTTTACGTCTGGGACGC
 L V G L S I L A N T F V P K E M Q T L R -
 1501 TGTGGCTTTGGCATGTCTGGGAATCGGCTGTTCTGCTGCTACTTTTCCAGTGTGTGCTGT + 1560
 ACACCGAAACCGTACAGACCCTTAGCCGACAAGACGACGATGAAAAAGGTCACAACGACA
 V A L A C L G I G C S A A T F S S V A V -
 1561 TCACTTCATTTGAACTCATCCCCACTGTTCTCAGGGCAAGAGCTTCAGGAATAGATTTAAC + 1620
 AGTGAAGTAACTTGAGTAGGGGTGACAAGAGTCCCGTTCTCGAAGTCCTTATCTAAATTG
 H F I E L I P T V L R A R A S G I D L T -
 1621 GGCTAGTAGGATTGGAGCAGCACTGGCTCCCCCTTGTATGACCTTAACGGTATTTTTTAC + 1680
 CCGATCATCCTAACCTCGTCGTGACCGAGGGGAGAACTACTGGAATTGCCATAAAAAATG
 A S R I G A A L A P L L M T L T V F F T -

FIGURE 6
 Sheet 3 of 5

1681 CACTTTGCCATGGATCATTTATGGAATCTTCCCCATCATTTGGTGGCCTTATTGTCTTCCT
 -----+-----+-----+-----+-----+ 1740
 GTGAAACGGTACCTAGTAAATACCTTAGAAGGGGTAGTAACCACCGGAATAACAGAAGGA

 T L P W I I Y G I F P I I G G L I V F L -

 1741 CCTACCAGAAACCAAGAATCTGCCTTTGCCTGACACCATCAAGGATGTGGAAAATCAAAA
 -----+-----+-----+-----+-----+ 1800
 GGATGGTCTTTGGTTCTTAGACGGAACGGACTGTGGTAGTTCCTACACCTTTTAGTTTT

 L P E T K N L P L P D T I K D V E N Q K -

 1801 AAAAAATCTCAAGGAAAAGGCATAAAAAATGATTGCTACACAAAAGTGACCAAATTTTAAG
 -----+-----+-----+-----+-----+ 1860
 TTTTTTAGAGTTCCTTTTCCGTATTTTTACTAACGATGTGTTTTCACTGGTTTAAATTC

 K N L K E K A *

 1861 AAGCCTTCATGAGCTGATTGGTGGGGAAATTCAGAAAAAAAAATACAGGAAAAGAACACA
 -----+-----+-----+-----+-----+ 1920
 TTCGGAAGTACTCGACTAACCACCCCTTTAAGTCTTTTTTTTTATGTCCTTTTCTGTGT

 CCAGAAGGGTTTTTTTCCCTACAACCAGCAAGAACATATATTAGATACATGAATCTCAAT
 1921 -----+-----+-----+-----+-----+ 1980
 GGTCTTCCCAAAAAAAGGGATGTTGGTTCGTTCTGTATATAATCTATGTACTTAGAGTTA

 TATAATTATGGCATTAATTTGCATTTTATTTCAAAAATTAAGTGTGGGGACATGTAATCT
 1981 -----+-----+-----+-----+-----+ 2040
 ATATTAATACCGTAATTAAACGTAAAAATAAGTTTTAATTGAACACCCCTGTACATTAGA

 CTTGAGCAATCTGATATTTTTGGGAAGTCCTTTAAAAAGTTACAAATTTATCAATAAATT
 2041 -----+-----+-----+-----+-----+ 2100
 GAACTCGTTAGACTATAAAAAACCCTTCAGGAAATTTTCAATGTTTAAATAGTTATTTAA

 ACTAGTAGATAAGATGATTCAGAAACAAAGGAAAAATCACAGAATTAGGATGTGGCTGGCT
 2101 -----+-----+-----+-----+-----+ 2160
 TGATCATCTATTCTACTAAGTCTTTGTTTCCTTTTAGTGTCTTAATCCTACACCGACCGA

 TGGTGTATGAAGCACCATGTGATGAATTCATAAAGTTGCAAAAGTCAAAACAATACTGTA
 2161 -----+-----+-----+-----+-----+ 2220
 ACCACATACTTCGTGGTACACTACTTAAGTATTTCAACGTTTTCAGTTTTGTTATGACAT

 CATGCAACCAGAAATCAAATTAATCCAGAAATAGAGACCTATATAAATGCATTTAATAC
 2221 -----+-----+-----+-----+-----+ 2280
 GTACGTTGGTCTTTAGTTTAATTTAGGTCTTTATCTCTGGATATATTTACGTAAATTATG

 ATGATACTTTTGACATATTAAGCCATTGGAAAACGGAAGGATTAGATACTTAAATAACAT
 2281 -----+-----+-----+-----+-----+ 2340
 TACTATGAAAACGTGATAATTTCGGTAACCTTTTGCCTTCCTAATCTATGAATTTATTGTA

 TGCTATCTCTTTGTAAATACAGTCACTAAATGATGTAGTTACTTTTCCATGGTGGAATT
 2341 -----+-----+-----+-----+-----+ 2400
 ACGATAGAGAAACATTTATGTCAGTGATTTACTACAATCAATGAAAAGGTACCACCTTAA

FIGURE 6
 Sheet 4 of 5

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TTAATTACTTTTTCTTTGTAATTTTTCTCTCTGTATATTTTAAACAAATAGCTGGTATAG
2401 -----+-----+-----+-----+-----+-----+ 2460
AATTAATGAAAAAGAAACATTAAAAAGAGAGACATATAAAATTTGTTTATCGACCATATC

TTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCAGGTTTCAAGCAATTTT
2461 -----+-----+-----+-----+-----+-----+ 2520
AAATGTTATAATATTTCTATAACAAGTTTAACTTCCCGTTTCCGGTCCAAGTCGTTAAAA

CAAACGTATGTACATTTAATAAAATAACTATAAATTAAAAAATTATATTTCAAATGATG
2521 -----+-----+-----+-----+-----+-----+ 2580
GTTTGACATACATGTAAATTATTTTATTGATATTTAATTTTTTAATATAAAGTTTACTAC

TGACTAATAAATGAAAGTACATATAGTAGTAAAGTAATTTCAAGCAAACCTATATAACCA
2581 -----+-----+-----+-----+-----+-----+ 2640
ACTGATTATTTACTTTTCATGTATATCATCATTTTCATTAAAGTCCGTTTGGATATATTGGT

AAATATAAACTTTTCATTTTAAACAGCAAAAAAAAAAAAAAAAAAAAA
2641 -----+-----+-----+-----+-----+-----+ 2684
TTTATATTTGAAAGTAAATTTGTCGTTTTTTTTTTTTTTTTTTTTT

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Transport of μ AH by OAT 1 in Hela

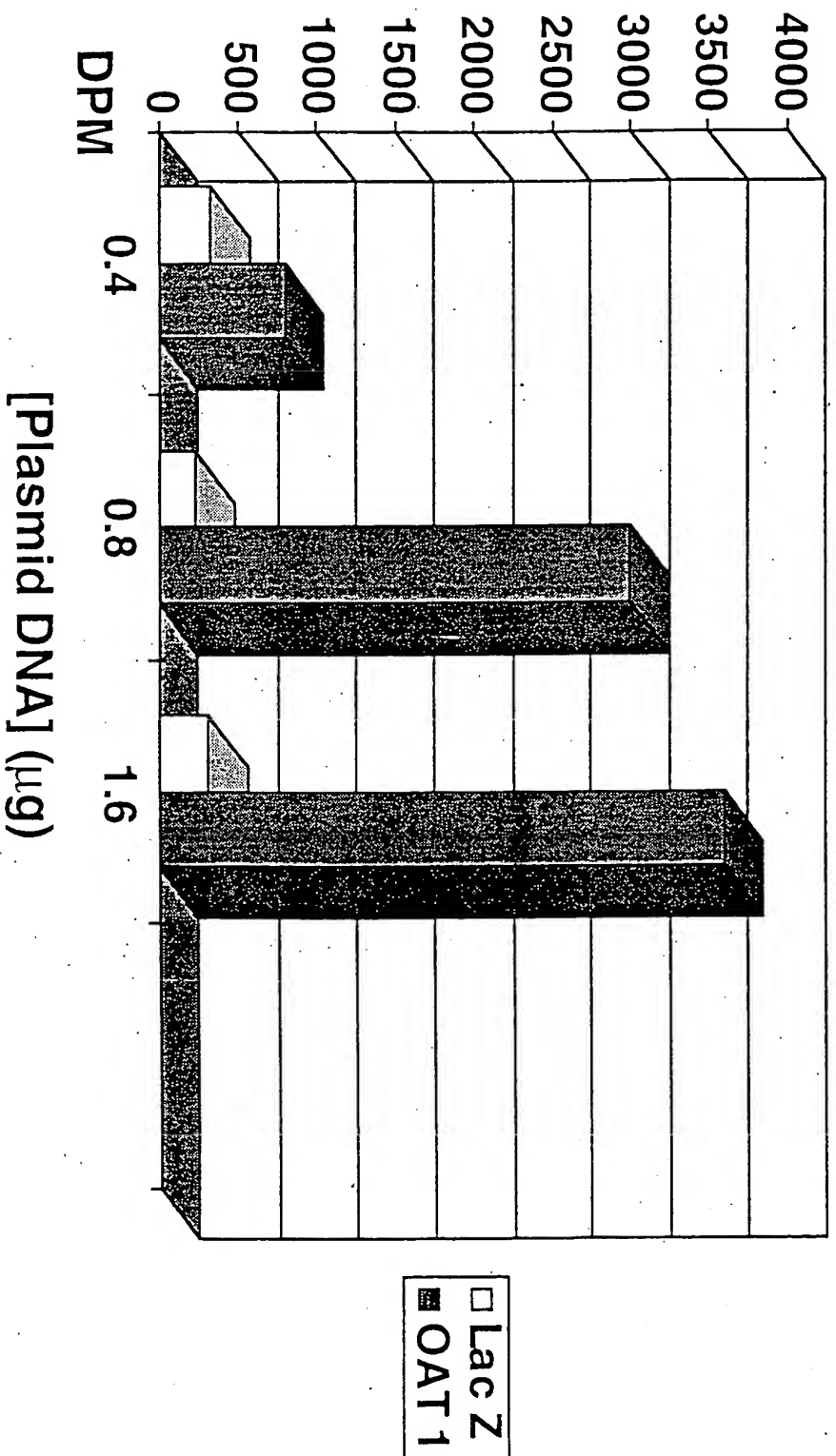


FIGURE 7

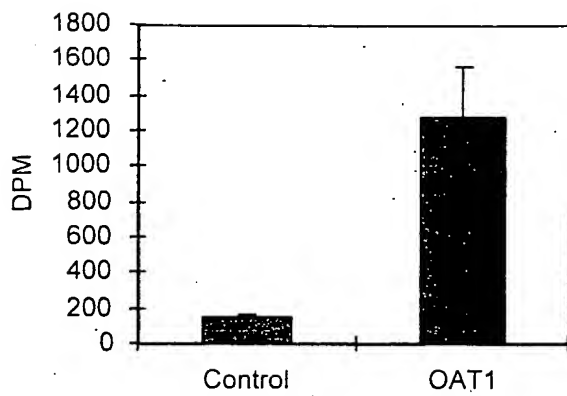


FIGURE 8

PAH Uptake by OAT2 EcR Cell Line

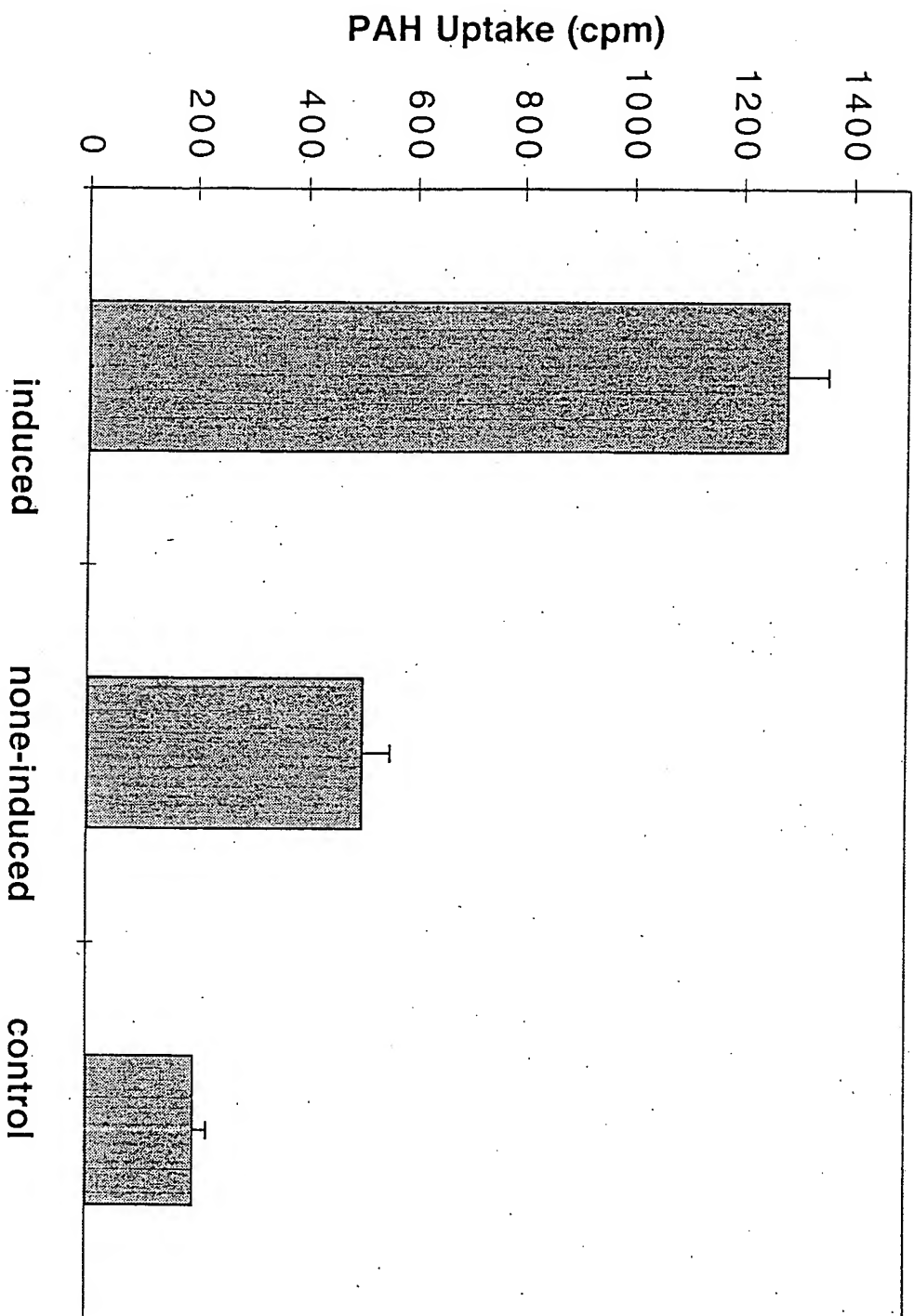


FIGURE 10





PAH Transport by EcR293-OAT2A

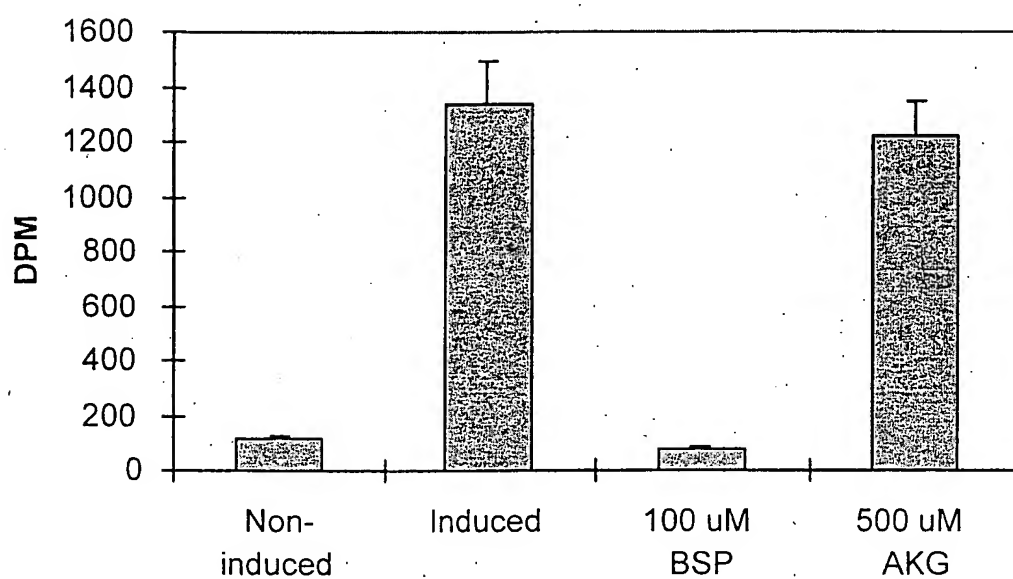


FIGURE 11